

SEQUENCE LISTING

<110> Enerbäck, Sven
Krook, Katarina
Rondahl, Lena
Wasserman, Wyeth

<120> PROMOTER SEQUENCES

<130> 13425-042001

<150> SE 0004102-0
<151> 2000-11-09

<150> US 60/238,897
<151> 2000-10-10

<150> SE 0003435-5
<151> 2000-09-26

<160> 24

<170> FastSEQ for Windows Version 4.0

```
<210> 1
<211> 6458
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (2235) . . . (3737)

<400> 1	cctttggctt	tgaattgatc	aggagacaaa	gataatgcat	ctacatttc	gtcttctgtt	60
	cttttatgg	aaataagtgg	cacccccat	tgccctctag	tcgcctccc	gaagcgaaga	120
	ggccgaagcg	aagaggcctg	gtgggtgtc	tcaacatcct	tttgctgaga	atcgaatacg	180
	cagccatga	acagccagga	agggtgcaag	gaaacctgaa	atacaaatgt	tctccctgaa	240
	gccctctcc	ctgcccacc	agaccagcaa	cttccaaaat	tctgcccgtg	tttagcccttg	300
	ttaaagggtt	gtctcactcc	ttcaggaaa	gtggaaaag	gggatctgt	tattgaggtg	360
	tggaaggaat	aaataatcag	tccacaaaata	aacaaaactgt	ccgggattcc	tagagggaaag	420
	gagaaaatcct	tgaaggagat	ccaagtgcgt	ccaggtctgc	ctgccaata	atatcatccc	480
	gaagggatct	tgaaccgtt	gcaatcaacc	gctcaccagg	tcttcccacg	gagcgcgctc	540
	ccttaactcac	cctaccacc	caacaaaaca	aaaaaaaggc	tgaardatata	aaaagcaact	600
	tggaggctcc	cagggggacg	ttgccaggag	caggaggcag	ggacagcgcc	ctagggctgg	660
	tgtagcgcc	cggcgccggc	ctgggcacg	gaaaacgtcc	acgcttggtg	cccgcggtgc	720
	gccccgtca	ttgcgcgcgc	cttcgagcca	agcccccgcg	gaaaacaggc	tcgggtttct	780
	cctcgacggg	cccaggaact	cggctctgcc	tgccccgggt	gggtcgctgc	attgtcccg	840
	tctctggga	gtgcggggtc	agcttggtag	agggaaattt	tacctggaa	aagggagacg	900
	agtttcaag	ctgaagttgg	taggctgcga	gtgtccacgc	gggagacgaa	agggggaaat	960
	agcagagtc	cttcaccctt	ttccccaaac	cccacaaaac	tgctcgacgc	gacgcggatg	1020
	atctaccgaa	ttcccccgca	attcgagga	ttaagttgtc	agtcagcagc	ttgtctacctt	1080
	ccccctatg	cactccgctg	cctggctcct	cggcgggag	cgagggaaac	ttagttgt	1140
	gggttacct	ctaaaacctc	gatagttat	ccttgacgac	cccgagcctg	gaaactccct	1200
	gtttagtatt	aattatttga	ttaaataagt	ataacatcca	ggagaggccc	tgccattcca	1260
	atccagcgcg	tttgccttttgc	aatccattac	acccggggcc	ccataattaq	qaaatctaata	1320

tattcgcttc atcactcatt aataagaaaa atgtcccagg atcattgcta cttacaaggt	1380
ctttgggaga gatattttac tctattaatc cattctattt tatatttcaa attgatttt	1440
tttaacagag gaaagtggct atcttttgc tttgggcatg tggggccatt caccaaaatg	1500
tgatcataaaa ataaattttataaagatata actttttaaa aagtttcaa gtgaagacgg	1560
agtcggccgca gaggccgggg cggccgggtc ttagagccga cggattcctg cgctcctcgc	1620
cccgattggc gccggactcc tctcagctgc cgggtgattt gctcaaagtt cgggagggg	1680
gcgtggcccg aggaaagtaa aaactcgctt tcagcaagaa gactttgaa actttccca	1740
atccctaaaaa gggacttggc ctctttctt gggctcagcg gggcagccgc tcggaccccg	1800
gcgcgtgac ctcggggctt gccgattcgc tgggggctt gagagcctcc tgcccccctc	1860
ctcgccggg cggagggtcc accttggtcc ccaggccgcg gcgtctccgc tgggtccgcg	1920
gccgcggcc tccccggcgtt gccggccgcg ggtcctggag ccagcgagga gcggggccgg	1980
cgctgcgtt gcccggggcg cggccctccag gatgcgcata cggccgggtcc gctgaaagcg	2040
cgcgcggctg ctggggccga gcgacgacga cggcgcaccc tcgccccggga ggctgccagg	2100
agaccggggc cggccctccc gtcggccctt tctggggcc tggctcttc gcgcgtcttc	2160
gctctcaggg cccccctcgc tccccggcc gcagtccgtg cgcgagggcg cggcgagcc	2220
gtctcggaaag cagc atg cag gcg cgc tac tcc gtg tcc gac ccc aac gcc	2270
Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala	
1 5 10	
ctg gga gtg gtg ccc tac ctg agc gag cag aat tac tac cgg gct gcg	2318
Leu Gly Val Val Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala	
15 20 25	
ggc agc tac ggc ggc atg gcc agc ccc atg ggc gtc tat tcc ggc cac	2366
Gly Ser Tyr Gly Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His	
30 35 40	
ccg gag cag tac agc gcg ggg atg ggc cgc tcc tac gcg ccc tac cac	2414
Pro Glu Gln Tyr Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His	
45 50 55 60	
cac cac cag ccc gcg gcg cct aag gac ctg gtg aag ccg ccc tac agc	2462
His His Gln Pro Ala Ala Pro Lys Asp Leu Val Lys Pro Pro Tyr Ser	
65 70 75	
tac atc gcg ctc atc acc atg gcc atc cag aac gcg ccc gag aag aag	2510
Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Glu Lys Lys	
80 85 90	
atc acc ttg aac ggc atc tac cag ttc atc atg gac cgc ttc ccc ttc	2558
Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe	
95 100 105	
tac cgg gag aac aag cag ggc tgg cag aac agc atc cgc cac aac ctc	2606
Tyr Arg Glu Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn Leu	
110 115 120	
tcg ctc aac gag tgc ttc gtc aag gtg ccc cgc gac gac aag aag ccc	2654
Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro	
125 130 135 140	
ggc aag ggc agt tac tgg acc ctg gac ccg gac tcc tac aac atg ttc	2702
Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe	
145 150 155	
gag aac ggc agc ttc ctg cgg cgc cgg cgg cgc ttc aaa aag aag gac	2750
Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Phe Lys Lys Asp	

160	165	170	
gtg tcc aag gag aag gag gag cg ^g gcc cac ctc aag gag cc ^g ccc cc ^g Val Ser Lys Glu Lys Glu Glu Arg Ala His Leu Lys Glu Pro Pro Pro			2798
175	180	185	
g ^c g g ^c g tcc aag g ^g c g ^c c cc ^g acc ccc cac cta g ^c g g ^a c g ^c c ccc Ala Ala Ser Lys Gly Ala Pro Ala Thr Pro His Leu Ala Asp Ala Pro			2846
190	195	200	
aag gag g ^c c gag aag aag gtg gtg atc aag agc gag g ^c g g ^c g tcc cc ^g Lys Glu Ala Glu Lys Lys Val Val Ile Lys Ser Glu Ala Ala Ser Pro			2894
205	210	215	220
g ^c g ctg cc ^g gtc atc acc aag gtg gag ac ^g ctg agc ccc gag agc g ^c g Ala Leu Pro Val Ile Thr Lys Val Glu Thr Leu Ser Pro Glu Ser Ala			2942
225	230	235	
ctg c ^a g g ^g c agc cc ^g cc ^g agc g ^c g g ^c cc tcc ac ^g ccc g ^c c tcc ccc Leu Gln Gly Ser Pro Arg Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro			2990
240	245	250	
g ^a c g ^g t tc ^g ctg cc ^g gag cac cac g ^c c g ^c g ccc aac g ^g g ctg cct Asp Gly Ser Leu Pro Glu His His Ala Ala Pro Asn Gly Leu Pro			3038
255	260	265	
g ^g c ttc agc gtg gag aac atc atg acc ctg cga ac ^g tc ^g cc ^g cc ^g g ^g c Gly Phe Ser Val Glu Asn Ile Met Thr Leu Arg Thr Ser Pro Pro Gly			3086
270	275	280	
g ^g a gag ctg agc cc ^g g ^g g g ^c c g ^c g g ^c cc ctg gtg gtg cc ^g cc ^g Gly Glu Leu Ser Pro Gly Ala Gly Arg Ala Gly Leu Val Val Pro Pro			3134
285	290	295	300
ctg g ^c g ctg cca tac g ^c c g ^c c g ^c g ccc g ^c c tac g ^c c cag cc ^g Leu Ala Leu Pro Tyr Ala Ala Pro Pro Ala Ala Tyr Gly Gln Pro			3182
305	310	315	
tgc gct cag g ^g c ctg gag g ^c c g ^g g g ^c c g ^g g tac cag tgc agc Cys Ala Gln Gly Leu Glu Ala Gly Ala Gly Gly Tyr Gln Cys Ser			3230
320	325	330	
atg cga g ^c g atg agc ctg tac acc g ^g g g ^c c gag c ^g g cc ^g g ^c g cac atg Met Arg Ala Met Ser Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Met			3278
335	340	345	
tgc gtc cc ^g ccc g ^c c ctg gac gag g ^c c ctc tc ^g gac cac cc ^g agc g ^g c Cys Val Pro Pro Ala Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly			3326
350	355	360	
ccc ac ^g tc ^g ccc ctg agc g ^c t ctc aac ctc g ^c c g ^c cc cag gag g ^g c Pro Thr Ser Pro Leu Ser Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly			3374
365	370	375	380
g ^c g ctc g ^c c g ^c c ac ^g g ^g c cac cac c ^g ac c ^g ac c ^g ac c ^g ac Ala Leu Ala Ala Thr Gly His His His Gln His His Gly His His His			3422
385	390	395	

ccg cag gcg ccg ccc ccg gct ccc cag ccc cag ccg acg ccg Pro Gln Ala Pro Pro Pro Pro Pro Ala Pro Gln Pro Gln Pro Thr Pro	3470
400 405 410	
cag ccc ggg gcc gcc gcg cag gcg gcc tcc tgg tat ctc aac cac Gln Pro Gly Ala Ala Ala Gln Ala Ala Ser Trp Tyr Leu Asn His	3518
415 420 425	
agc ggg gac ctg aac cac ctc ccc ggc cac acg ttc gcg gcc cag cag Ser Gly Asp Leu Asn His Leu Pro Gly His Thr Phe Ala Ala Gln Gln	3566
430 435 440	
caa act ttc ccc aac gtg cgg gag atg ttc aac tcc cac cgg ctg ggg Gln Thr Phe Pro Asn Val Arg Glu Met Phe Asn Ser His Arg Leu Gly	3614
445 450 455 460	
att gag aac tcg acc ctc ggg gag tcc cag gtg agt ggc aat gcc agc Ile Glu Asn Ser Thr Leu Gly Glu Ser Gln Val Ser Gly Asn Ala Ser	3662
465 470 475	
tgc cag ctg ccc tac aga tcc acg ccg cct ctc tat cgc cac gca gcc Cys Gln Leu Pro Tyr Arg Ser Thr Pro Pro Leu Tyr Arg His Ala Ala	3710
480 485 490	
ccc tac tcc tac gac tgc acg aaa tac tgacgtgtcc cgggacacctcc Pro Tyr Ser Tyr Asp Cys Thr Lys Tyr	3757
495 500	
cctccccggc ccgctccggc ttgcgttccc agccccgacc caaccagaca attaaggggc tgccagagacg caaaaaagaa acaaaaacatg tccaccaacc ttttctcaga cccgggagca	3817 3877
gagagccggc acgctagccc ccagccgtct gtgaagagcg caggttaactt taattcggccg ccccgttct gggatcccg gaaaccctc caaagggacg cagcccaaca aaatgagttat	3937 3997
tggtcttaaa atccccctcc cctaccagga cggctgtgct gtgctcgacc tgagcttca aaagtttaagt tatggaccca aatcccatag cgagccctta gtgacttct gttaggggtcc	4057 4117
ccataggtgt atgggggtct ctatagataa tatatgtgct gtgtgtaatt ttaaatttct ccaaaccgtgc tgtacaatg tgtggatttg taatcaggtct atttgttgt tggtgttgc	4177 4237
gttcagagcc attaatataa tatttaagt tgagttcaact ggataagttt ttcatcttgc ccaaaccattt ctaactgcca aattgaattc aagaaaaccca tttgggtttt gtttctgtta	4297 4357
caattatgag atataattct ttttccattt gtaggtcttt tacaaaacaa gaaaataatt tatttttttggata aagaagtcaa gtatctgata ctttttattt acaaagtgtg	4417 4477
atggttttgt atagtaggtt ccaccctgag tattcctaaa agaaaaaaaaaaa aaaaaaaagct taaaaactct aacttcatct gtgttgc tttttttttt tacgtggct taatcgttacttaccta	4537 4597
aaataaaaccc atgttggttt ttctgccccaa agtttggaca gtgttgc tttgttgc tttttacaaa cgaggtgtgt ttgcaaaaccc acctgcttgc attatttttt ttacacaggt	4657 4717
gggtatatgt gtagacacat aaaaacgacc agagaatagg agcacacacc tgctgttt tttagtgaca gaaaaaggct tttgattat tttttttttt cactcttagga tttttttttt	4777 4837
tcgagaaaacc gcccagttgg agggggctgc ctgaaggacc ggaccatgag tttgcgtga tgcattttct taaatgcaca aaaacatgct aattgtcaaa acaaacagtgc ccactccatc	4897 4957
tcagtgtcca gccgtccccca gttttaggagg tgaaggaagg gaagaataaa cattttccgt ttgctaaactg caaccccgagg tgagtcctgc tttccccca ttttataaaa tttgagcctc	5017 5077
tttgccctgct ttaatagttt tccagagaat ttgaactggg ccaatgaagg tctgaagg acggattttc tagcggttga tatccatccc ctttagcgcc cagatcagag gggatattca	5137 5197
gacttttatta cttctcaatg tcatgtctaa atctacaccc tcacatcgact gaaaaatttt aaaacccat tacccttcaa aaataattt tgatattttt agagttctaa attcaagttt	5257 5317
ttcaatatgt taaataatag agattttttt ttgttttcaa tgtaatatc tcgttttta catttttaat agtaacatag ttttggaa atgttagctga cggaaatggct ttattatcta	5377 5437

tttcaatggc	tgaagtccac	caactccctg	ctggccctca	tgtgtgaatt	tggggaccaa	5497
agcttcatca	attcccaccc	cagcagggtga	gctgtacctt	gctaattgtcg	aagttcttg	5557
tgagcttaac	gtttcaagac	cagatgattt	tgctaaaggt	gattttgctt	gatgcagttgg	5617
cgctgaacgt	aaccgggtg	tttttgcgt	gttgccttca	acatggcact	ttatctccac	5677
gctatgttga	aatagaatta	ggggaaagctt	aaagcataat	aattgtcccc	acatgtgcaa	5737
cacagactct	ttcaatctgt	ggcccccagag	gtggcacaca	gttaagactt	gcccggctgtc	5797
tcattcttt	tcataatgtg	cgggttcccg	ggtgtccggg	tgctagactt	tcagcaggcc	5857
ccaggccaga	cgggcttgg	ttgagtgaaac	aggaggagga	agtttaaggag	gtaggggtgg	5917
ggagagaccc	tctccaagct	gcagaagaag	gtggcccaag	ctccttcgcct	gcgtctgccc	5977
tgatggttc	atttacttc	tgctcgcttc	atgctatttgc	ccccaggaga	agaggagagt	6037
attccagacg	gtaagcggc	tggcttttc	ccttccctag	acgtttaaa	gaaatcttc	6097
tgaaagcttg	ccctcatcgt	aagcttgaa	accgttgggt	tcctgttagt	ggcgaggggct	6157
gagagacacg	cggagaaata	aaggagagcg	acgggtgtggc	tgagagcccc	caggctctgt	6217
gttgaacta	agctgggctt	ttgcacccctt	aggaagcctt	tttaaagaag	tcctgtctgt	6277
tgggggccgg	aagcccaagt	gagtggccct	tgtggaggtt	atcgggaggg	gtctttacca	6337
ctccttgggg	aacgtgggca	acggggggat	tgtatctgaa	gctttattca	ggtcttcggc	6397
ggcagcagag	tggagaacca	ggcccttagt	gtgtagcggc	ctggggattt	ttggactcat	6457
c						6458

<210> 2

<211> 501

<212> PRT

<213> *Homo sapiens*

<400> 2

Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala Leu Gly Val Val
1 5 10 15

Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala Gly Ser Tyr Gly
20 25 30

Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His Pro Glu Gln Tyr
 35 40 45

Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His His His Gln Pro
 50 55 60

Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn
 100 105 110
 Lys Gln Gly Trp Gln Asp Ser Ile Arg His Asp Lys Ser Lys Asp Gly

115 120 125
 Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser

Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asp Met Phe Glu Asn Gly Ser
 130 135 140

145	150	155	160												
Phe	Leu	Arg	Arg	Arg	Arg	Arg	Phe	Lys	Lys	Lys	Asp	Val	Ser	Lys	Glu

165 170 175
 Lys Glu Glu Arg Ala His Leu Lys Glu Pro Pro Pro Ala Ala Ser Lys

180 185 190
Gly Ala Pro Ala Thr Pro His Leu Ala Asp Ala Pro Lys Glu Ala Glu

195	200	205
Lys Lys Val Val Ile Lys Ser Glu Ala Ala Ser Pro Ala Leu Pro Val		

```

210           215           220
Ile Thr Lys Val Glu Thr Leu Ser Pro Glu Ser Ala Leu Gln Gly Ser

```

225 230 235 240
 Pro Arg Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro Asp Gly Ser Leu
 245 250 255 260

245 250 255

Pro Glu His His Ala Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val
 260 265 270
 Glu Asn Ile Met Thr Leu Arg Thr Ser Pro Pro Gly Gly Glu Leu Ser
 275 280 285
 Pro Gly Ala Gly Arg Ala Gly Leu Val Val Pro Pro Leu Ala Leu Pro
 290 295 300
 Tyr Ala Ala Ala Pro Pro Ala Ala Tyr Gly Gln Pro Cys Ala Gln Gly
 305 310 315 320
 Leu Glu Ala Gly Ala Ala Gly Gly Tyr Gln Cys Ser Met Arg Ala Met
 325 330 335
 Ser Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Met Cys Val Pro Pro
 340 345 350
 Ala Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly Pro Thr Ser Pro
 355 360 365
 Leu Ser Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly Ala Leu Ala Ala
 370 375 380
 Thr Gly His His His Gln His His Gly His His His Pro Gln Ala Pro
 385 390 395 400
 Pro Pro Pro Pro Ala Pro Gln Pro Gln Pro Thr Pro Gln Pro Gly Ala
 405 410 415
 Ala Ala Ala Gln Ala Ala Ser Trp Tyr Leu Asn His Ser Gly Asp Leu
 420 425 430
 Asn His Leu Pro Gly His Thr Phe Ala Ala Gln Gln Gln Thr Phe Pro
 435 440 445
 Asn Val Arg Glu Met Phe Asn Ser His Arg Leu Gly Ile Glu Asn Ser
 450 455 460
 Thr Leu Gly Glu Ser Gln Val Ser Gly Asn Ala Ser Cys Gln Leu Pro
 465 470 475 480
 Tyr Arg Ser Thr Pro Pro Leu Tyr Arg His Ala Ala Pro Tyr Ser Tyr
 485 490 495
 Asp Cys Thr Lys Tyr
 500

<210> 3
 <211> 4158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187) ... (1437)

<400> 3
 cctttggctt tgaattgatc aggagacaaa gataatgcat ctacatttc gtcttctgtt 60
 cttttattgg aaataagtgg cacgccccat tgccttctag tcgcctcccc gaagcgaaga 120
 ggcggaaagcg aagaggcctg gtgggttgtc tcaacatcct tttgctgaga atcgaatacg 180
 cagccg atg aac agc cag gaa ggg tgc aag gaa acc ttg aac ggc atc 228
 Met Asn Ser Gln Glu Gly Cys Lys Glu Thr Leu Asn Gly Ile
 1 5 10

tac cag ttc atc atg gac cgc ttc ccc ttc tac cgg gag aac aag cag 276
 Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn Lys Gln
 15 20 25 30

ggc tgg cag aac agc atc cgc cac aac ctc tcg ctc aac gag tgc ttc 324
 Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu Cys Phe
 35 40 45

gtc aag gtg ccc cgc gac gac aag aag ccc ggc aag ggc agt tac tgg		372	
Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser Tyr Trp			
50	55	60	
acc ctg gac ccg gac tcc tac aac atg ttc gag aac ggc agc ttc ctg		420	
Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser Phe Leu			
65	70	75	
cg ^g cgc cg ^g cg ^g cgc ttc aaa aag aag gac gtg tcc aag gag aag gag		468	
Arg Arg Arg Arg Phe Lys Lys Lys Asp Val Ser Lys Glu Lys Glu			
80	85	90	
gag cg ^g gcc cac ctc aag gag ccg ccc ccg gc ^g gc ^g tcc aag ggc gcc		516	
Glu Arg Ala His Leu Lys Glu Pro Pro Ala Ala Ser Lys Gly Ala			
95	100	105	110
ccg gcc acc ccc cac cta gc ^g gac gc ^g ccc aag gag gc ^g gag aag aag		564	
Pro Ala Thr Pro His Leu Ala Asp Ala Pro Lys Glu Ala Glu Lys Lys			
115	120	125	
gtg gtg atc aag agc gag gc ^g gc ^g tcc ccg gc ^g ctg ccg gc ^g atc acc		612	
Val Val Ile Lys Ser Glu Ala Ala Ser Pro Ala Leu Pro Val Ile Thr			
130	135	140	
aag gtg gag acg ctg agc ccc gag agc gc ^g ctg cag gg ^g agc ccg cg ^g		660	
Lys Val Glu Thr Leu Ser Pro Glu Ser Ala Leu Gln Gly Ser Pro Arg			
145	150	155	
agc gc ^g gc ^g tcc acg ccc gc ^g tcc ccc gac ggt tc ^g ctg ccg gag		708	
Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro Asp Gly Ser Leu Pro Glu			
160	165	170	
cac cac gc ^g gc ^g ccc aac ggg ctg cct gc ^g ttc agc gtg gag aac		756	
His His Ala Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val Glu Asn			
175	180	185	190
atc atg acc ctg cga acg tc ^g ccg gg ^g gag ctg agc ccg ggg		804	
Ile Met Thr Leu Arg Thr Ser Pro Pro Gly Gly Glu Leu Ser Pro Gly			
195	200	205	
gcc gga cg ^g gc ^g gc ^g ctg gtg ccg ccg ctg gc ^g ctg cca tac gc ^g		852	
Ala Gly Arg Ala Gly Leu Val Val Pro Pro Leu Ala Leu Pro Tyr Ala			
210	215	220	
gcc gc ^g ccg ccc gc ^g tac gg ^g cag ccg tgc gct cag gg ^g ctg gag		900	
Ala Ala Pro Pro Ala Ala Tyr Gly Gln Pro Cys Ala Gln Gly Leu Glu			
225	230	235	
gcc ggg gcc gcc ggg gg ^g tac cag tgc agc atg cga gc ^g atg agc ctg		948	
Ala Gly Ala Ala Gly Gly Tyr Gln Cys Ser Met Arg Ala Met Ser Leu			
240	245	250	
tac acc ggg gcc gag cg ^g ccg gc ^g cac atg tgc gtc ccg ccc gc ^g ctg		996	
Tyr Thr Gly Ala Glu Arg Pro Ala His Met Cys Val Pro Pro Ala Leu			
255	260	265	270

gac gag gcc ctc tcg gac cac ccg agc ggc ccc acg tcg ccc ctg agc Asp Glu Ala Leu Ser Asp His Pro Ser Gly Pro Thr Ser Pro Leu Ser 275 280 285	1044
gct ctc aac ctc gcc ggc cag gag ggc gcg ctc gcc gcc acg ggc Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly Ala Leu Ala Ala Thr Gly 290 295 300	1092
cac cac cac cag cac cac cac ccg cag gcg ccg ccc His His Gln His His Gly His His Pro Gln Ala Pro Pro Pro 305 310 315	1140
ccg ccg gct ccc cag ccc cag ccg acg ccg cag ccc ggg gcc gcc gcg Pro Pro Ala Pro Gln Pro Gln Pro Thr Pro Gln Pro Gly Ala Ala Ala 320 325 330	1188
gcg cag gcg gcc tcc tgg tat ctc aac cac agc ggg gac ctg aac cac Ala Gln Ala Ala Ser Trp Tyr Leu Asn His Ser Gly Asp Leu Asn His 335 340 345 350	1236
ctc ccc ggc cac acg ttc gcg gcc cag cag caa act ttc ccc aac gtg Leu Pro Gly His Thr Phe Ala Ala Gln Gln Thr Phe Pro Asn Val 355 360 365	1284
cgg gag atg ttc aac tcc cac cgg ctg ggg att gag aac tcg acc ctc Arg Glu Met Phe Asn Ser His Arg Leu Gly Ile Glu Asn Ser Thr Leu 370 375 380	1332
ggg gag tcc cag gtg agt ggc aat gcc agc tgc cag ctg ccc tac aga Gly Glu Ser Gln Val Ser Gly Asn Ala Ser Cys Gln Leu Pro Tyr Arg 385 390 395	1380
tcc acg ccg cct ctc tat cgc cac gca gcc ccc tac tcc tac gac tgc Ser Thr Pro Pro Leu Tyr Arg His Ala Ala Pro Tyr Ser Tyr Asp Cys 400 405 410	1428
acg aaa tac tgacgtgtcc cgggacacctcc cctcccccggc ccgctccggc Thr Lys Tyr 415	1477
ttcgcttccc agccccgacc caaccagaca attaaggggc tgcagagacg caaaaaagaa acaaaacatg tccaccaacc ttttctcaga cccgggagca gagagcgggc acgctagccc ccagccgtct gtgaagagcg caggttaactt taattcgccg cccctttct gggatcccag gaaacccctc caaagggacg cagcccaaca aaatgagtat tggctttaaa atccccctcc cctaccagga cggctgtgtc gtgctcgacc tgagctttca aaagtttaagt tatggaccca aatcccatag cgagccctta gtgactttct gttaggggtcc ccataggtgt atgggggtct ctatagataa tatatgtgtc gtgtgttaatt taaaatttct ccaaccgtgc tgtacaaatag tgtggatttg taatcaggct attttgtgt tggtgttgg tttcagagcc attaatataa tatttaaagt tgagttcaact ggataagttt ttcatcttgc ccaaccattt ctaactgcca aattgaattc aagaaaacgga tgggtttt gttccctgta caattatgag atataattct ttttcccatt gtaggtcttt tacaaaacaa gaaaataatt tatttttttggatgatggata aagaagtcaa gtatctgata ctttttattt acaaagtgtg atgggtttgt atagtaggtt ccaccctgag tattcctaaa agaaaaaaaaaaaaaaagct taaaaactct aacttcatct gtgtttgtct tacgtggtct taatcgttgc acttaccta aaataaaccctt atgttggttt ttctgccccaa agtttggaca gtgtgtttgt gttgttgcat ttttacaaa cgaggtgtgt ttgcaaaccc acctgctttg attatttttg ttacacaggt gggatatgt gttagacacat aaaaacgacc agagaatagg agcacacacc tgctgtctg ttttagtgaca gaaaaaggct	1537 1597 1657 1717 1777 1837 1897 1957 2017 2077 2137 2197 2257 2317 2377 2437 2497

tttgattaat	tttaaaatcc	cactctagga	tttttcttt	tcgagaaaacc	gcccagttgg	2557
agggggctgc	ctgaaggacc	ggaccatgag	tttgcgtga	tgcattttct	taaatgcaca	2617
aaaacatgct	aattgtcaaa	acaaaacagtg	ccactccatc	tcagtgtcca	gcccgtcccc	2677
gtttaggagg	tgaaggaagg	gaagaataaa	catttcccg	ttgctaactg	caacccaggg	2737
tgagtcctgc	tttccccca	ttttataaaa	tttgagcctc	tttgctgtct	ttaatagttt	2797
tccagagaat	ttgaactggg	ccaatgaagg	tctgaagggg	acggattttc	tagcgttga	2857
tatccatccc	ccttagcggc	cagatcagag	gggaatttca	gactttatta	cttctcaatg	2917
tcatgtctaa	atctacaccc	tcatcgcagt	aaaaaattt	aaaacctcat	tacccttcaa	2977
aaataattta	tgatatttt	agagttctaa	attcaagttt	ttcaatatgt	taaataatag	3037
agattatttt	ttgtttcaa	tgttaatatac	tcgtctttt	catttttaat	agtaacatag	3097
tttttgtgaa	atgtagctga	cgaaatggct	tttatatcta	tttcaatggc	tgaagtcac	3157
cactcccctg	ctggcctcta	tgtgtgaatt	tggggaccaa	agcttcatca	attcccaccc	3217
cagcaggtga	gctgtaccc	gctaatgctg	aagttcttg	tgagcttaac	gtttcaagac	3277
cagatgattt	tgctaaagg	gatttgc	tgatgcagtgg	cgctgaacgt	aacccgggtg	3337
tttttgtcg	ttgttttca	acatggact	ttatctccac	gctatgtga	aatagaatta	3397
ggggaaagctt	aaagcataat	aattgtcccc	acatgtgca	cacagactct	ttcaatctgt	3457
ggccccagag	gtggcacaca	gttaagactt	ggcggctgtc	tcatttttt	tcataatgtg	3517
cgggttcccg	ggtgtccggg	tgctagactt	tcagcaggcc	ccaggccaga	cgggcttgg	3577
ttgagtgaac	aggaggagga	agttaggag	gtaggggtgg	ggagagaccc	tctccaagct	3637
gcagaagaag	gtggcccaag	ctccttg	gctgtcgcc	tgatggttc	atttacttc	3697
tgctcgcttc	atgctatttt	ccccaggaga	agaggagagt	attccagacg	gtaagcgagc	3757
tggcttttc	cctccctag	acgtttaaa	gaaatcttc	tgaaagcttgc	ccctcatcg	3817
aagcttcaa	accgttgg	tcctgttagt	ggcgagg	gagagacacg	cgaggaaata	3877
aaggagagcg	acgggtgtggc	tgagagcccc	caggtctgt	gttggaaacta	agctgggtt	3937
ttgcaccc	tttgggg	tttgggg	tttgggg	tttgggg	tttgggg	3997
gagtggccct	tgtggaggtt	atcgggaggg	gtcttacca	ctccctgggg	aacgtggca	4057
acggggggat	tgtatctgaa	gttttattca	ggtcttcggc	ggcagcagag	tggagaacca	4117
ggcccttagt	gtgtagcggc	ctggggattt	tggactcat	c		4158

<210> 4
<211> 417
<212> PRT
<213> Homo sapiens

<400> 4

Met	Asn	Ser	Gln	Glu	Cys	Lys	Glu	Thr	Leu	Asn	Gly	Ile	Tyr	Gln	
1														15	
Phe	Ile	Met	Asp	Arg	Phe	Pro	Phe	Tyr	Arg	Glu	Asn	Lys	Gln	Gly	
		20						25						30	
Gln	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	Asn	Glu	Cys	Phe	Val	Lys
			35					40						45	
Val	Pro	Arg	Asp	Asp	Lys	Lys	Pro	Gly	Lys	Gly	Ser	Tyr	Trp	Thr	Leu
			50				55							60	
Asp	Pro	Asp	Ser	Tyr	Asn	Met	Phe	Glu	Asn	Gly	Ser	Phe	Leu	Arg	Arg
					65			70			75				80
Arg	Arg	Arg	Phe	Lys	Lys	Asp	Val	Ser	Lys	Glu	Lys	Glu	Glu	Arg	
					85			90						95	
Ala	His	Leu	Lys	Glu	Pro	Pro	Pro	Ala	Ala	Ser	Lys	Gly	Ala	Pro	Ala
					100			105						110	
Thr	Pro	His	Leu	Ala	Asp	Ala	Pro	Lys	Glu	Ala	Glu	Lys	Val	Val	
					115			120						125	
Ile	Lys	Ser	Glu	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Val	Ile	Thr	Lys	Val
					130			135						140	
Glu	Thr	Leu	Ser	Pro	Glu	Ser	Ala	Leu	Gln	Gly	Ser	Pro	Arg	Ser	Ala
					145			150			155				160
Ala	Ser	Thr	Pro	Ala	Gly	Ser	Pro	Asp	Gly	Ser	Leu	Pro	Glu	His	His
					165			170						175	

Ala Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val Glu Asn Ile Met
 180 185 190
 Thr Leu Arg Thr Ser Pro Pro Gly Gly Glu Leu Ser Pro Gly Ala Gly
 195 200 205
 Arg Ala Gly Leu Val Val Pro Pro Leu Ala Leu Pro Tyr Ala Ala Ala
 210 215 220
 Pro Pro Ala Ala Tyr Gly Gln Pro Cys Ala Gln Gly Leu Glu Ala Gly
 225 230 235 240
 Ala Ala Gly Gly Tyr Gln Cys Ser Met Arg Ala Met Ser Leu Tyr Thr
 245 250 255
 Gly Ala Glu Arg Pro Ala His Met Cys Val Pro Pro Ala Leu Asp Glu
 260 265 270
 Ala Leu Ser Asp His Pro Ser Gly Pro Thr Ser Pro Leu Ser Ala Leu
 275 280 285
 Asn Leu Ala Ala Gly Gln Glu Gly Ala Leu Ala Ala Thr Gly His His
 290 295 300
 His Gln His His Gly His His His Pro Gln Ala Pro Pro Pro Pro Pro
 305 310 315 320
 Ala Pro Gln Pro Gln Pro Thr Pro Gln Pro Gly Ala Ala Ala Gln
 325 330 335
 Ala Ala Ser Trp Tyr Leu Asn His Ser Gly Asp Leu Asn His Leu Pro
 340 345 350
 Gly His Thr Phe Ala Ala Gln Gln Thr Phe Pro Asn Val Arg Glu
 355 360 365
 Met Phe Asn Ser His Arg Leu Gly Ile Glu Asn Ser Thr Leu Gly Glu
 370 375 380
 Ser Gln Val Ser Gly Asn Ala Ser Cys Gln Leu Pro Tyr Arg Ser Thr
 385 390 395 400
 Pro Pro Leu Tyr Arg His Ala Ala Pro Tyr Ser Tyr Asp Cys Thr Lys
 405 410 415
 Tyr

<210> 5
 <211> 6021
 <212> DNA
 <213> Mus musculus

<220>
 <221> exon
 <222> (1649) ... (438)

<400> 5
 ctcgagtcaa aggtagcaca cataaaacct attttgcgc ttcgtacgt caagcaatgc 60
 cactaaagtt tcctcaccgg ccaaagctga aacagttagt tctaattctt caaaggcctt 120
 tgccgaaaat ctaaagggggg tggggggcta tgggtggtggc gtgggggggg ggtcgagaa 180
 gaagaaagac tgagacaaat gtttatctg tgccttctt ccctacccaa ccggaccaac 240
 aacttccaga aggttctgcg aggcatacgg ccattccgtt gggacatctc ggtgcttctg 300
 aggaagcggg ccgagcaggg atccgatgac gactggagat gttgaaggaa taaataccag 360
 tccacaaaata aacaaaactgt ccccggtt cctagagggaa aggagcacgc ttgaaggctg 420
 gggaaactccg agtcgctgtg cgtcaagggtt ggcataaaat taaaaaaaaaaa aaaagtccctt 480
 cagttaccag gcccctctaag gagccctgg tcctcagctc accttataa aactcgtaa 540
 aacaaaacagc ctgaaataca gtcaatttac aggtacccaa agatgctgac cgcggagtg 600
 gacccacgccc gggcccccggc aacagctagg gaagcgggtc cgaggctaca cagtgcccg 660
 ctccttgcg tttccagtga cgaagccggc gatggagtgc aggcttggag ctccccacgc 720
 cgaacgggaa caccagctcc cgggggctgg ctgccttgc ctaacctcca gacagcgctt 780
 tcataggtgg ggagaaggaa gaggccggga tggatggcag ggaaagctag ccctcgtcta 840

tgccggagag gagaccagga aagcaacagt tggttcacg cgcttccctg aaccccacga	900
aattgtttgg aggactcaga tggatcacct aagtagcagc gaagacgaag gaccaatgg	960
tccttaggtg ttaccttccc agtttggcat tcccactaag ccttccctcc cagcccgacc	1020
ccgtcgtgaa ggggagagga accgaattct ccaacccggc ctcccttgc ggccttccct	1080
caacctggaa gcgtcctgt aattatccat cactgcattc aacaggccct acacgctcag	1140
tccgtttgtc ctgaacccat tacaactagg ccccgataat taagaaatct aattattcgc	1200
ctcttcatcc attaataata ataaaaaaaaa aatctccagg ctcttccta cttacaaggt	1260
cttggggca aatctctgcc caacttcattc aattcgatgt tatatttcaa actaaactc	1320
tttttatttt ccaaaggaaac agggtttta attttgcgc tggacacgtg gtctcgtaa	1380
acaaaatgtg ataataaaaat aaaatttt aagatgtaac tcattttaa aagtcctcaa	1440
gttaacttga gctggggggg ggggagatct ggctaagagc atctgggtct tagagccgac	1500
ggattcaggc gctcctcggt ttgattggtg ccatccttct cgcaagctgcc agatgatgg	1560
tgcaaaacttc ctggaggggg cgccgcctga agaaaagtaaa aactcgctt gagccagaag	1620
actttgaaa cttttcccaa tccctaaaag ggactttgtct tcttttccg ggctcgcccg	1680
cgcagcctct ccggacccta gctcgctgac gctgcgggct gcagtttcc tggcggggcc	1740
cgagagccgc tgtctccctt tctagcactc ggaagggctg gtgtcgctcc acggtcgcgc	1800
gtggcgtctg tgccgcgc ctagggctgc caccgcctaa gccgagagtg cgccgcgc	1860
ggggccgcct gccgtgcacc cttcaggatg ccgcgcgc cggtaggtg aacccgagcg	1920
ccggcgtctt cgcgcgtgg accgcgaggc tgcccccagt cgggctgcc tgcgcgc	1980
cgtcccttcc tgctctccctg ctccggccct cgctcgccgc gggccgcagt cggtcgcgc	2040
aggcggcgcac cggggtctg ggacgcagca tgcaggcgcc ttactcgta tcggacccca	2100
acgccttggg agtggtaccc tattttagtg agcaaaaacta ctaccggcg gccggcagct	2160
acggccgcattt ggccagcccc atgggcgtct actccggcca cccggagcg tacggcgc	2220
gcatggcccg ctccctacgcg ccctaccacc accagccgc ggcgcgcctaa gacctgggtga	2280
agccccccta cagctatata gcgcctatca ccatggcgat ccagaacgcg ccagagaaga	2340
agatcactctt gaacggcattc taccagttca tcatggaccc ttcccttc taccgcgaga	2400
acaagcaggg ctggcagaac agcatccgc acaacctgtc actcaatgag tgctcgta	2460
aagtggcgcg cgacgacaag aagccggca agggcagcta ctggacgc gacccggact	2520
cctacaacat gttcgagaat ggcagcttcc tgcggcggcg gcggcgcttc aagaagaagg	2580
atgtgcccggg ggacaaggag gagcggggccc acctcaaggaa gcccgcctcg accacggcca	2640
agggcgctcc gacagggacc ccggtagctg acggggccca ggagggccgag aagaaagtgc	2700
tggtaagag cgaggcggcg tccccgcgc tgccggtcat caccaagggtg gagacgctga	2760
gcccccgaggg agcgctgcag gccagtcgc gcagcgcattc ctccacgc gcaagggtccc	2820
cagacggctc gtcggcggag caccacgcg cggcgcttaa cgggctgcc ggcttcagcg	2880
tggagaccat catgacgc tgcacgc ctcggggccg cgatctgagc ccagcggccg	2940
cgcgcccgccg ctgggtggc ccaccgcg cactgcata cgccgcagcg ccacccggcc	3000
cttacacgca gccgtgcgcg cagggcctgg aggctgcggg ctccgcggc taccagtgc	3060
gtatgcggc tatgagtctg tacacggggcc cggagcggcc cgccgcacgtg tgcttcgc	3120
ccgcgcttgcg cggggctctg tcggaccacc cgagcggccc cggctcccg ctggcggccc	3180
tcaacctcgc agcggtcag gaggcgcgt tggggccctc ggttaccac caccagcatc	3240
acggccaccc ctaccgcg ggcgcaccgc cggccccc gcccctccc ggcgcgcgc	3300
ccgcacccca ggcacccctcc tggtatctga accacggccgg ggacctgagc cacctcccc	3360
gccacacgtt tgcaacccaa cagcaactt tccccacgt cggggagatg ttcaactcgc	3420
acgggtctagg actggacaac tcgtccctcg gggagtcctc ggtgagcaat gcgcgcgtc	3480
agctccctta tcgagctacg ccgtccctct accgcacgc agcccccctac tcttacgact	3540
gcaccaaata ctgaggctgt ccagtcgc ctagccccag gaccgcaccg gcttcgc	3600
ctccatggga accttctcg acggagccgc agaaagcgc ggaagcgcc cctctctc	3660
aaccaggagc agagagctcc gtgcaactcg caggttaactt atccgcagct cagtttggaa	3720
tctcagcgcg tccctctaag gggatgcag cccagcaaaa cgaataacag atttttttt	3780
taattcttc ccctacccag atgctgcgc tgctccctg gggcttcata gattagctt	3840
tggaccaaac ccatagggac ccctaattgac ttctgtggag attctccacg ggcgcacag	3900
gtctctccgg ataaggtgcc ttctgttaac gagtgccgat ttgtaccag gctatttgt	3960
tcttgcggc agccttaat ataatttt aagttgtgtc cactggataa ggtttcgct	4020
tgcccaactg ttactgccttccatttca agaaacgtgt gtgggtctt tctcccccacg	4080
tcaccatgt aaaataggtc cttcccaaa ctgttaggtct ttacaaaac aagaaaataaa	4140
tttattttttt tggtgtgtt ggataacgaa attaagtatac ggataactttt aatttaggaa	4200
gtgcacggct ttgtacagta gatgcacatc ggggtattcc aaaaacacac caaaagactt	4260

taaaatttca atctcacctg	tgtttgttctt atgtgatctc	agtgttgtat ttaccttaaa	4320
ataaaccgt gttgttttc	tgcccaaagt tcggacagag	tctttgtt cttgaatttt	4380
aaaaggaaa ttgttagtaag	ccagttgtga ttgattttt	tgatgcaggt tggcctggt	4440
acgtggatgc atatacagt	tacaggacga tggagctctc	gattagtaat agaaggggct	4500
cttgatttgt tgaactatcc	cgtcctgaga tattttgtt	ttctgctcgaa gtaatctga	4560
gaaactgttc tccatccaca	cacggacagg gctgcctgag	ggcaacgtcc tgctggcctg	4620
ttaacgaaat gcttgcggg	atgcagaaaa ctgttgccaa	ttgtcaaaac aaaaatggtgt	4680
caccctgtct cggtgtccag	ctgtcctctg ttagagggga	gaaaccgaga aaggacaaac	4740
ggcctgcagc ttgctaact	cagcgtagca ggagcctggg	tgagtgcctg gctccctcca	4800
tttccttaga tgcggacttg	ttgcccctgt tggcgtttt	agagtgcag caagaagcaa	4860
agagggttgg taggtctctg	gtatttaact gccggcttt	ggatcagatt agaagtgaat	4920
ttcagtcga tttatttctt	aattttggct ttaaatattt	tactccggcg tggtgaaaaa	4980
agaaggccact gtgcgcctcc	agcatgatat ttagcgctg	aaatggctct gggtttcagc	5040
atgctaagta acaggagatt	atttttctt tgattctt	atttcatttc tttaaaaaaaa	5100
aaaaaggaaa tagatcgaaa	caaactctct	aaaatgtacc tggctggctg ggggtgggtc	5160
cttaccaatc tgctgcctga	aagatacagc ttcagcacag	gcctgcgtgt tggactttag	5220
gcatatcatg gattcccacg	ccagttgta acctggactg	tgctaatggaa agttcttct	5280
gcacagaaca ttagggccag	gaggaggcag ggaccggga	gggggggtgga ctttgcaggt	5340
catctgctta gcttagtgg	ggccacgggt	taacacgtat atagtgttac tggactttag	5400
tccaaatccc atatctgtgc	tgtttgcgtg	tagaattttgg ggaggttctt gatgatacta	5460
ccctaccgt gtatgtaaa	cagttttca acctgcagtg	ccagaatgtg acccacactt	5520
cagttatcttc cataaagtgg	ggggactaag aactggacag	gggtgcgtg gggggggca	5580
ggccagggtgt atcttggttc	ctgagcagag cagagagtt	aggaagggtt cgggagatct	5640
ctgggtcctc ccaacactgg	tttcattttgcatggctc	ttcaaacctc ttgccccagg	5700
agaagcgagc tttgtccaag	ccagctggct cgctccttc	ccagatgttt taggggcctc	5760
cctgaaagct tgcctcctc	ttaagattca gaactcctga	cccaggaaa gataggaggc	5820
tttggatg ggagctttt	tttaaagagg accgttctcg	ttctcaagta ggtagctaga	5880
gagaagcccc ctggagcagg	ccctacttgt gactgtcagg	gaaccagggt tgggttttag	5940
gtttttccca gcctcccaag	agcagcggtg	tgaaaaaaatg cggtcctggg aaaagtttgtt	6000
ctgggtgtt gcttcctcga	g		6021

<210> 6
<211> 2712

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (422) ... (1903)

<400> 6

aggactttg cttcttttc	cgggctcgcc cgcgacgcct	ctccggaccc tagctcgctg	60
acgctgcggg ctgcagttt	cctggcgaaa cccgagagcc	gctgtctctt tttcttagcac	120
tcggaaaggcc tgggtgcgt	ccacggctgc	gcgtggcgta tggccgcca gctcagggt	180
gccaccgcgc aagccgagag	tgcgcggcca	gcggggccgc ctgcgtgca cccttcagga	240
tggccatccg cccggctggc	tgaacccgag	gcggggcgta ttccgcgtt ggaccgag	300
gctgccccga gtcggggctg	cctgcatcgc	tccgtccctt cctgcctctc tgctccgggc	360
ctcgctcgcc gcggggccgc	gtcggtgcgc	gcaggcggcg accggggatc tgggacgcag	420
c atg cag gcg cgt tac	tcg gta tcg	gac ccc aac gcc ctg gga gtg gta	469

Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala Leu Gly Val Val
1 5 10 15

ccc tat ttg agt gag	caa aac tac tac	cg gcg gcc agc tac ggc	517
Pro Tyr Leu Ser Glu	Gln Asn Tyr Tyr	Arg Ala Ala Gly Ser Tyr Gly	
20	25	30	

ggc atg gcc agc ccc	atg ggc gtc tac tcc	ggc cac ccg gag cag tac	565
---------------------	---------------------	-------------------------	-----

Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His Pro Glu Gln Tyr			
35	40	45	
ggc gcc ggc atg ggc cgc tcc tac gcg ccc tac cac cac cag ccc gcg			613
Gly Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His His Gln Pro Ala			
50	55	60	
gcg ccc aag gac ctg gtg aag ccg ccc tac agc tat ata gcg ctc atc			661
Ala Pro Lys Asp Leu Val Lys Pro Pro Tyr Ser Tyr Ile Ala Leu Ile			
65	70	75	80
acc atg gcg atc cag aac gcg cca gag aag aac atc act ctg aac ggc			709
Thr Met Ala Ile Gln Asn Ala Pro Glu Lys Lys Ile Thr Leu Asn Gly			
85	90	95	
atc tac cag ttc atc atg gac cgt ttc ccc tac cgc gag aac aag			757
Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn Lys			
100	105	110	
cag ggc tgg cag aac agc atc cgc cac aac ctg tca ctc aat gag tgc			805
Gln Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu Cys			
115	120	125	
ttc gtg aaa gtg ccg cgc gac gac aag aag ccg ggc aag ggc agc tac			853
Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser Tyr			
130	135	140	
tgg acg ctc gac ccg gac tcc tac aac atg ttc gag aat ggc agc ttc			901
Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser Phe			
145	150	155	160
ctg cgg cgg cgg cgg cgc ttc aag aag aag gat gtg ccc aag gac aag			949
Leu Arg Arg Arg Arg Phe Lys Lys Lys Asp Val Pro Lys Asp Lys			
165	170	175	
gag gag cgg gcc cac ctc aag gag ccg ccc tcg acc acg gcc aag ggc			997
Glu Glu Arg Ala His Leu Lys Glu Pro Pro Ser Thr Thr Ala Lys Gly			
180	185	190	
gct ccg aca ggg acc ccg gta gct gac ggg ccc aag gag gcc gag aag			1045
Ala Pro Thr Gly Thr Pro Val Ala Asp Gly Pro Lys Glu Ala Glu Lys			
195	200	205	
aaa gtc gtg gtt aag agc gag gcg gcg tcc ccc gcg ctg ccg gtc atc			1093
Lys Val Val Val Lys Ser Glu Ala Ala Ser Pro Ala Leu Pro Val Ile			
210	215	220	
acc aag gtg gag acg ctg agc ccc gag gga gcg ctg cag gcc agt ccg			1141
Thr Lys Val Glu Thr Leu Ser Pro Glu Gly Ala Leu Gln Ala Ser Pro			
225	230	235	240
ccg agc gca tcc tcc acg ccc gca ggt tcc cca gac ggc tcg ctg ccg			1189
Arg Ser Ala Ser Ser Thr Pro Ala Gly Ser Pro Asp Gly Ser Leu Pro			
245	250	255	
gag cac cac gcc gcg cct aac ggg ctg ccc ggc ttc agc gtg gag			1237
Glu His His Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val Glu			

260

265

270

1285

acc atc atg acg ctg cgc acg tcg cct ccg ggc ggc gat ctg agc cca
 Thr Ile Met Thr Leu Arg Thr Ser Pro Pro Gly Gly Asp Leu Ser Pro
 275 280 285

1333

gcg gcc gcg cgc gcc ggc ctg gtg cca ccg ctg gca ctg cca tac
 Ala Ala Ala Arg Ala Gly Leu Val Val Pro Pro Leu Ala Leu Pro Tyr
 290 295 300

1381

gcc gca gcg cca ccc gcc gct tac acg cag ccg tgc gcg cag ggc ctg
 Ala Ala Ala Pro Pro Ala Ala Tyr Thr Gln Pro Cys Ala Gln Gly Leu
 305 310 315 320

1429

gag gct gcg ggc tcc gcg ggc tac cag tgc agt atg cgg gct atg agt
 Glu Ala Ala Gly Ser Ala Gly Tyr Gln Cys Ser Met Arg Ala Met Ser
 325 330 335

1477

ctg tac acc ggg gcc gag cgg ccc gcg cac gtg tgc gtt ccg ccc gcg
 Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Val Cys Val Pro Pro Ala
 340 345 350

1525

ctg gac gag gct ctg tcg gac cac ccg agc ggc ccc ggc tcc ccg ctc
 Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly Pro Gly Ser Pro Leu
 355 360 365

1573

ggc gcc ctc aac ctc gca gcg ggt cag gag ggc gcg ttg ggg gcc tca
 Gly Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly Ala Leu Gly Ala Ser
 370 375 380

1621

ggt cac cac cac cag cat cac ggc cac ctc cac ccg cag gcg cca ccg
 Gly His His His Gln His His Gly His Leu His Pro Gln Ala Pro Pro
 385 390 395 400

1669

ccc gcc ccg cag ccc cct ccc gcg ccg cag ccc gcc acc cag gcc acc
 Pro Ala Pro Gln Pro Pro Ala Pro Gln Pro Ala Thr Gln Ala Thr
 405 410 415

1717

tcc tgg tat ctg aac cac ggc ggg gac ctg agc cac ctc ccc ggc cac
 Ser Trp Tyr Leu Asn His Gly Gly Asp Leu Ser His Leu Pro Gly His
 420 425 430

1765

acg ttt gca acc caa cag caa act ttc ccc aac gtc ccg gag atg ttc
 Thr Phe Ala Thr Gln Gln Thr Phe Pro Asn Val Arg Glu Met Phe
 435 440 445

1813

aac tcg cac ccg cta gga ctg gac aac tcg tcc ctc ggg gag tcc cag
 Asn Ser His Arg Leu Gly Leu Asp Asn Ser Ser Leu Gly Glu Ser Gln
 450 455 460

1861

gtg agc aat gcg agc tgt cag ctg ccc tat cga gct acg ccg tcc ctc
 Val Ser Asn Ala Ser Cys Gln Leu Pro Tyr Arg Ala Thr Pro Ser Leu
 465 470 475 480

1903

tac cgc cac gca gcc ccc tac tct tac gac tgc acc aaa tac
 Tyr Arg His Ala Ala Pro Tyr Ser Tyr Asp Cys Thr Lys Tyr
 485 490

tgaggctgtc	cagtccgctc	cagccccagg	accgcaccgg	cttcgcctcc	tccatggaa	1963
ccttcttcga	cgagccgca	gaaagcgacg	gaaagcgccc	ctctctcaga	accaggagca	2023
gagagctccg	tgcaactcgc	aggtaactta	tccgcagctc	agtttgagat	tcagcgagt	2083
ccctctaagg	gggatgcagc	ccagcaaaac	gaaatacaga	ttttttttt	aattccttcc	2143
cctacccaga	tgctgcgcct	gctcccttgg	ggcttcatacg	attagcttat	ggaccaaacc	2203
catagggacc	cctaattgact	tctgtggaga	ttctccacgg	gcgcagagg	tctctccgga	2263
taaggtgcct	tctgtaaacg	agtgcggatt	tgtaaccagg	ctatttgtt	cttgcggcaga	2323
gcctttaata	taatatttaa	agttgtgtcc	actggataag	gtttcgctt	gccccactgt	2383
tactgccaaa	tgaaattcaa	gaaacgtgtg	tgggtctttt	ctccccacgt	caccatgata	2443
aaataagggcc	ctccccaaac	tgttaggtctt	ttacaaaaca	agaaaataat	ttatttttt	2503
gttgggtttg	gataacgaaa	ttaagtatcg	gatacttttta	attttaggaag	tgcatggctt	2563
tgtacagtag	atgccatctg	gggttattcca	aaaacacacc	aaaagacttt	aaaatttcaa	2623
tctcacctgt	gtttgtctta	tgtgatctca	gtgttgtatt	taccttaaaa	taaacccgtg	2683
ttgtttttct	gccccaaaaaa	aaaaaaaaaa				2712

<210> 7

<211> 494

<212> PRT

<213> Mus musculus

<400> 7

Met	Gln	Ala	Arg	Tyr	Ser	Val	Ser	Asp	Pro	Asn	Ala	Leu	Gly	Val	Val
1						5					10			15	
Pro	Tyr	Leu	Ser	Glu	Gln	Asn	Tyr	Tyr	Arg	Ala	Ala	Gly	Ser	Tyr	Gly
							20				25			30	
Gly	Met	Ala	Ser	Pro	Met	Gly	Val	Tyr	Ser	Gly	His	Pro	Glu	Gln	Tyr
							35				40			45	
Gly	Ala	Gly	Met	Gly	Arg	Ser	Tyr	Ala	Pro	Tyr	His	His	Gln	Pro	Ala
							50				55			60	
Ala	Pro	Lys	Asp	Leu	Val	Lys	Pro	Pro	Tyr	Ser	Tyr	Ile	Ala	Leu	Ile
							65				70			75	
Thr	Met	Ala	Ile	Gln	Asn	Ala	Pro	Glu	Lys	Lys	Ile	Thr	Leu	Asn	Gly
							85				90			95	
Ile	Tyr	Gln	Phe	Ile	Met	Asp	Arg	Phe	Pro	Phe	Tyr	Arg	Glu	Asn	Lys
							100				105			110	
Gln	Gly	Trp	Gln	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	Asn	Glu	Cys
							115				120			125	
Phe	Val	Lys	Val	Pro	Arg	Asp	Asp	Lys	Lys	Pro	Gly	Lys	Gly	Ser	Tyr
							130				135			140	
Trp	Thr	Leu	Asp	Pro	Asp	Ser	Tyr	Asn	Met	Phe	Glu	Asn	Gly	Ser	Phe
							145				150			155	
Leu	Arg	Arg	Arg	Arg	Arg	Phe	Lys	Lys	Lys	Asp	Val	Pro	Lys	Asp	Lys
							165				170			175	
Glu	Glu	Arg	Ala	His	Leu	Lys	Glu	Pro	Pro	Ser	Thr	Thr	Ala	Lys	Gly
							180				185			190	
Ala	Pro	Thr	Gly	Thr	Pro	Val	Ala	Asp	Gly	Pro	Lys	Glu	Ala	Glu	Lys
							195				200			205	
Lys	Val	Val	Val	Lys	Ser	Glu	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Val	Ile
							210				215			220	
Thr	Lys	Val	Glu	Thr	Leu	Ser	Pro	Glu	Gly	Ala	Leu	Gln	Ala	Ser	Pro
							225				230			235	
Arg	Ser	Ala	Ser	Ser	Thr	Pro	Ala	Gly	Ser	Pro	Asp	Gly	Ser	Leu	Pro
							245				250			255	
Glu	His	His	Ala	Ala	Ala	Pro	Asn	Gly	Leu	Pro	Gly	Phe	Ser	Val	Glu
							260				265			270	
Thr	Ile	Met	Thr	Leu	Arg	Thr	Ser	Pro	Pro	Gly	Gly	Asp	Leu	Ser	Pro

275	280	285
Ala Ala Ala Arg Ala Gly Leu Val Val Pro Pro	Leu Ala Leu Pro Tyr	
290	295	300
Ala Ala Ala Pro Pro Ala Ala Tyr Thr Gln Pro	Cys Ala Gln Gly Leu	
305	310	315
Glu Ala Ala Gly Ser Ala Gly Tyr Gln Cys Ser	Met Arg Ala Met Ser	
325	330	335
Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Val	Cys Val Pro Pro Ala	
340	345	350
Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly	Pro Gly Ser Pro Leu	
355	360	365
Gly Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly	Ala Leu Gly Ala Ser	
370	375	380
Gly His His His Gln His His Gly His Leu His	Pro Gln Ala Pro Pro	
385	390	395
Pro Ala Pro Gln Pro Pro Pro Ala Pro Gln Pro	Ala Thr Gln Ala Thr	
405	410	415
Ser Trp Tyr Leu Asn His Gly Gly Asp Leu Ser	His Leu Pro Gly His	
420	425	430
Thr Phe Ala Thr Gln Gln Thr Phe Pro Asn Val	Arg Glu Met Phe	
435	440	445
Asn Ser His Arg Leu Gly Leu Asp Asn Ser Ser	Leu Gly Glu Ser Gln	
450	455	460
Val Ser Asn Ala Ser Cys Gln Leu Pro Tyr Arg	Ala Thr Pro Ser Leu	
465	470	475
Tyr Arg His Ala Ala Pro Tyr Ser Tyr Asp Cys	Thr Lys Tyr	
485	490	

<210> 8
 <211> 3289
 <212> DNA
 <213> Homo sapiens

<400> 8

gaattcggag gattaagttg tcagtcagca cgttgctacc ttccctctta tgcactccgc	60
tgcctggctc ctggcgcccc agcgaggaa actcagttt tagggtttac ctctaaaacc	120
tgcataaggaa atccttgcacg accccgagcc tggaaactcc ctgttgatga ttaattattt	180
gattaaataa gtataacatc caggagaggc cctgccattc caatccagcg cgtttgcctt	240
tgaatccatt acacctggc cccataatt aggaaatcta attattcgct tcatcactca	300
ttaataagaa aatgtccca ggatcattgc tacttacaag gtctttggga gagatatttt	360
actctattaa tccattctat tttatatttc aaattgatt ttttaacag aggaaagtgg	420
ctatctttt gtttggcca tggccca ttccacaaaa tgtgatcata aaataaaattt	480
taataagata taacttttta aaaagtttc aagtgaagac ggagtgcggc cggaggccgg	540
ggcggcgcccc tcttagagcc gacggattcc tgcgtccctc gccccgattt ggcggcgact	600
cctctcagct gccgggtgtat tggctcaaag ttccgggagg gggcggtggcc cgagggaaagt	660
aaaaactcgc tttcagcaag aagactttt aacttttcc caatccctaa aaggggacttgc	720
gcctttttt ctgggtctcg cggggcagcc gtcggaccc cggcgcgctg accctcgcccc	780
ctggcgattc gtcgggggt tggagagcct cctgcgcctt tcctcgcgcc ggcggaggg	840
ccaccttggt cccaggccg cggcgcttcc gtcgggtccg cggcgccccc cctgcccccg	900
ctggccggc cgggtcttgg agccagcgag gagcggggcc ggcgtgcgc ttggccgggg	960
cgcccccctcc aggatgcccga tccggccggc cgcgtgaaag cgcgcgcggcc tgctcgcccc	1020
gagcgacgac gaccgcgcac ctcgcggccg gaggctgcca ggagaccggg gccgcggcc	1080
ccgcctccct cctctccccc tctggctctc tgcgtctc tcgcgtctcg ggcggccctc	1140
gtccccccgg cccgactcg tgcgcggagg cggcgccggag cgcgtctcgaa agcagcatgc	1200
aggcgccgcta ctccgtgtcc gacccaaacg ccctggggagt ggtgcctac ctgagcgagc	1260
agaattacta cccggctcg ggcagctacg gccgcgtggc cagccccatg ggcgtctatt	1320
ccggccaccc ggagcgtac agcgcgggga tggccgctc ctacgcggcc taccaccacc	1380

accagccccgc	ggcgccctaag	gacctgggtga	agccggcccta	cagctacatc	gcgctcatca	1440
ccatggccat	ccagaacgcg	cccgagaaga	agatcacctt	gaacggcatc	taccagttca	1500
tcatggaccg	cttccccttc	taccgggaga	acaaggcaggg	ctggcagaac	agcatccgcc	1560
acaaccttc	gctcaacgag	tgcttcgtca	aggtgccccg	cgacgacaag	aagccggca	1620
agggcagtt	ctggaccctg	gaccggact	cctacaacat	gttcgagaac	ggcagcttcc	1680
tgccggcccg	gcccgccttc	aaaaagaagg	acgtgtccaa	ggagaaggag	gagcgggccc	1740
acctcaagga	gcccggcccg	gcccgttca	agggcgcddd	ggccacccccc	cacctagcgg	1800
acgccccaa	ggaggccgag	aagaaggtgg	tgatcaagag	cgaggccgccc	tccccggcgc	1860
tgccggtcat	caccaaggtg	gagacgctga	gccccgagag	cgcgctgcag	ggcagccccg	1920
gcagcgcggc	ctccacgccc	gcccgtccc	ccgacggttc	gctggcggag	caccacgccc	1980
cggcgcggaa	cgggctgcct	ggctttagcg	tgggagaacat	catgaccctg	cgaacgtcgc	2040
cgcggggcgg	agagctgagc	ccgggggccc	gacgcgcggg	cctgggtgt	ccgcccgttgg	2100
cgctgccata	cgcccgcgcg	ccgcccgcgc	cctacggcca	gcccgtgcgt	cagggccttgg	2160
aggccggggc	cgccgggggc	taccagtgc	gatgcgcagc	gatgagcctg	tacaccgggg	2220
ccgagcggcc	ggcgacatg	tgcgtcccgc	ccgcccctgg	cgaggccctc	tcggaccacc	2280
cgagcggccc	cacgtcgccc	ctgagcgctc	tcaacctcgc	cgccggccag	gagggcgcgc	2340
tcgcccac	gggccaccac	caccagcacc	acggccacca	ccacccgcag	gcccgcgcgc	2400
ccccgcggc	tccccagcccc	cagccgacgc	cgcagcccg	ggccgcccgc	gcccggcgg	2460
cctcttgta	tctcaaccac	agcggggacc	tgaaccaccc	ccccggccac	acgttcgcgg	2520
cccagcagca	aactttcccc	aacgtgcggg	agatgttcaa	ctccaccgg	ctggggatttgc	2580
agaactcgac	cctcggggag	tcccaggtga	gtggcaatgc	cagctgcag	ctgcccata	2640
gatccacgccc	gcctctctat	cgccacgcag	ccccctactc	ctacgactgc	acgaaataact	2700
gacgtgtccc	gggacctccc	ctccccggcc	cgctccggct	tcgcttccca	gccccgaccc	2760
aaccagacaa	ttaaggggct	gcagagacgc	aaaaaaagaaaa	caaaacatgt	ccaccaaccc	2820
tttctcagac	ccgggagcag	agagcgggca	cgctagcccc	cagccgtctg	tgaagagcgc	2880
aggttaacttt	aatcgccgc	cccgtttctg	ggatcccagg	aaaccctcc	aaagggaacgc	2940
agcccaacaa	aatgagtatt	ggtcttaaaa	tccccctccc	ctaccaggac	ggctgtgtcg	3000
tgctcgaccc	gagcttcaa	aagttaagtt	atggacccaa	atcccata	gagcccttag	3060
tgactttctg	taggggtccc	cataggtgt	tgggggtctc	tatagataat	atatgtgtcg	3120
tgtgttaattt	taaatttctc	caaccgtgt	gtacaaatgt	gtggatttgc	aatcaggcata	3180
ttttgttgtt	gttgttgtt	ttcagagcca	ttaatataat	atttaaagtt	gagttcactg	3240
gataagttt	tcatcttgcc	caaccatttc	taactgccaa	attgaattc		3289

<210> 9
<211> 1506
<212> DNA
<213> Homo

<220>
<221> CDS
<222> (1)...(1503)

<400> 9
atg cag gcg cgc tac tcc gtg tcc gac ccc aac gcc ctg gga gtg gtg 48
Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala Leu Gly Val Val
1 5 10 15

ccc tac ctg agc gag cag aat tac tac cg_g gct g_cg g_gc agc tac g_gc 96
 Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala Gly Ser Tyr Gly
 20 25 30

```

ggc atg gcc agc ccc atg ggc gtc tat tcc ggc cac ccg gag cag tac 144
Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His Pro Glu Gln Tyr
35 40 45

```

```
agc gcg ggg atg ggc cgc tcc tac gcg ccc tac cac cac cac cag ccc 192
Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His His His Gln Pro
```

50	55	60														
gcg	gct	aag	gac	ctg	gtg	aag	ccg	ccc	tac	agc	tac	atc	gct	ctc	240	
Ala	Ala	Pro	Lys	Asp	Leu	Val	Lys	Pro	Pro	Tyr	Ser	Tyr	Ile	Ala	Leu	
65					70					75					80	
atc	acc	atg	gcc	atc	cag	aac	gct	ccc	gag	aag	aag	atc	acc	ttg	aac	288
Ile	Thr	Met	Ala	Ile	Gln	Asn	Ala	Pro	Glu	Lys	Lys	Ile	Thr	Leu	Asn	
					85					90					95	
ggc	atc	tac	cag	ttc	atc	atg	gac	cgc	ttc	ccc	ttc	tac	cgg	gag	aac	336
Gly	Ile	Tyr	Gln	Phe	Ile	Met	Asp	Arg	Phe	Pro	Phe	Tyr	Arg	Glu	Asn	
					100					105					110	
aag	cag	ggc	tgg	cag	aac	agc	atc	cgc	cac	aac	ctc	tcg	ctc	aac	gag	384
Lys	Gln	Gly	Trp	Gln	Asn	Ser	Ile	Arg	His	Asn	Leu	Ser	Leu	Asn	Glu	
					115					120					125	
tgc	ttc	gtc	aag	gtg	ccc	cgc	gac	gac	aag	aag	ccc	ggc	aag	ggc	agt	432
Cys	Phe	Val	Lys	Val	Pro	Arg	Asp	Asp	Lys	Lys	Pro	Gly	Lys	Gly	Ser	
					130					135					140	
tac	tgg	acc	ctg	gac	ccg	gac	tcc	tac	aac	atg	ttc	gag	aac	ggc	agc	480
Tyr	Trp	Thr	Leu	Asp	Pro	Asp	Ser	Tyr	Asn	Met	Phe	Glu	Asn	Gly	Ser	
					145					150					160	
ttc	ctg	cg	cg	cg	cg	cg	ttc	aaa	aag	aag	gac	gtg	tcc	aag	gag	528
Phe	Leu	Arg	Arg	Arg	Arg	Arg	Phe	Lys	Lys	Lys	Asp	Val	Ser	Lys	Glu	
							165				170				175	
aag	gag	gag	cg	gg	cc	cc	ct	cc	aag	cg	cc	cc	g	cc	aa	576
Lys	Glu	Glu	Arg	Ala	His	Leu	Lys	Glu	Pro	Pro	Pro	Ala	Ala	Ser	Lys	
					180					185					190	
ggc	gcc	ccg	gg	cc	cc	cc	ct	g	cc	624						
Gly	Ala	Pro	Ala	Thr	Pro	His	Leu	Ala	Asp	Ala	Pro	Lys	Glu	Ala	Glu	
					195					200					205	
aag	aag	gt	gt	atc	aag	agc	gag	cg	cg	tcc	ccg	cg	ctg	ccg	gt	672
Lys	Lys	Val	Val	Ile	Lys	Ser	Glu	Ala	Ala	Ser	Pro	Ala	Leu	Pro	Val	
					210					215					220	
atc	acc	aag	gt	gag	ac	ctg	agc	ccc	gag	agc	cg	ctg	cag	ggc	agc	720
Ile	Thr	Lys	Val	Glu	Thr	Leu	Ser	Pro	Glu	Ser	Ala	Leu	Gln	Gly	Ser	
					225					230					240	
ccg	cgc	agc	cg	gg	cc	cc	cc	cc	cc	gac	gg	tc	cg	ct	768	
Pro	Arg	Ser	Ala	Ala	Ser	Thr	Pro	Ala	Gly	Ser	Pro	Asp	Gly	Ser	Leu	
							245			250					255	
ccg	gag	cac	cac	gg	cc	cc	aac	gg	ctg	cct	gg	ttc	agc	gt	816	
Pro	Glu	His	His	Ala	Ala	Ala	Pro	Asn	Gly	Leu	Pro	Gly	Phe	Ser	Val	
							260			265					270	
gag	aac	atc	atg	acc	ctg	cga	ac	tcg	ccg	ccg	gg	gag	ctg	agc	864	
Glu	Asn	Ile	Met	Thr	Leu	Arg	Thr	Ser	Pro	Pro	Gly	Gly	Glu	Leu	Ser	
							275			280					285	

<210> 10
<211> 501
<212> PRT
<213> Homo sapiens

<400> 10
Met Gln Ala Arg Tyr Ser Val Ser Asp Pro Asn Ala Leu Gly Val Val
1 5 10 15
Pro Tyr Leu Ser Glu Gln Asn Tyr Tyr Arg Ala Ala Gly Ser Tyr Gly
20 25 30
Gly Met Ala Ser Pro Met Gly Val Tyr Ser Gly His Pro Glu Gln Tyr
35 40 45
Ser Ala Gly Met Gly Arg Ser Tyr Ala Pro Tyr His His Gln Pro
50 55 60
Ala Ala Pro Lys Asp Leu Val Lys Pro Pro Tyr Ser Tyr Ile Ala Leu
65 70 75 80
Ile Thr Met Ala Ile Gln Asn Ala Pro Glu Lys Lys Ile Thr Leu Asn
85 90 95
Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe Pro Phe Tyr Arg Glu Asn
100 105 110
Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Glu
115 120 125
Cys Phe Val Lys Val Pro Arg Asp Asp Lys Lys Pro Gly Lys Gly Ser
130 135 140
Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn Met Phe Glu Asn Gly Ser
145 150 155 160
Phe Leu Arg Arg Arg Arg Phe Lys Lys Lys Asp Val Ser Lys Glu
165 170 175
Lys Glu Glu Arg Ala His Leu Lys Glu Pro Pro Pro Ala Ala Ser Lys
180 185 190
Gly Ala Pro Ala Thr Pro His Leu Ala Asp Ala Pro Lys Glu Ala Glu
195 200 205
Lys Lys Val Val Ile Lys Ser Glu Ala Ala Ser Pro Ala Leu Pro Val
210 215 220
Ile Thr Lys Val Glu Thr Leu Ser Pro Glu Ser Ala Leu Gln Gly Ser
225 230 235 240
Pro Arg Ser Ala Ala Ser Thr Pro Ala Gly Ser Pro Asp Gly Ser Leu
245 250 255
Pro Glu His His Ala Ala Ala Pro Asn Gly Leu Pro Gly Phe Ser Val
260 265 270
Glu Asn Ile Met Thr Leu Arg Thr Ser Pro Pro Gly Gly Glu Leu Ser
275 280 285
Pro Gly Ala Gly Arg Ala Gly Leu Val Val Pro Pro Leu Ala Leu Pro
290 295 300
Tyr Ala Ala Ala Pro Pro Ala Ala Tyr Gly Gln Pro Cys Ala Gln Gly
305 310 315 320
Leu Glu Ala Gly Ala Ala Gly Gly Tyr Gln Cys Ser Met Arg Ala Met
325 330 335
Ser Leu Tyr Thr Gly Ala Glu Arg Pro Ala His Met Cys Val Pro Pro
340 345 350
Ala Leu Asp Glu Ala Leu Ser Asp His Pro Ser Gly Pro Thr Ser Pro
355 360 365
Leu Ser Ala Leu Asn Leu Ala Ala Gly Gln Glu Gly Ala Leu Ala Ala
370 375 380
Thr Gly His His His Gln His His Gly His His His Pro Gln Ala Pro
385 390 395 400

Pro Pro Pro Pro Ala Pro Gln Pro Gln Pro Thr Pro Gln Pro Gly Ala
 405 410 415
 Ala Ala Ala Gln Ala Ala Ser Trp Tyr Leu Asn His Ser Gly Asp Leu
 420 425 430
 Asn His Leu Pro Gly His Thr Phe Ala Ala Gln Gln Gln Thr Phe Pro
 435 440 445
 Asn Val Arg Glu Met Phe Asn Ser His Arg Leu Gly Ile Glu Asn Ser
 450 455 460
 Thr Leu Gly Glu Ser Gln Val Ser Gly Asn Ala Ser Cys Gln Leu Pro
 465 470 475 480
 Tyr Arg Ser Thr Pro Pro Leu Tyr Arg His Ala Ala Pro Tyr Ser Tyr
 485 490 495
 Asp Cys Thr Lys Tyr
 500

<210> 11
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 11
 ttttttttac attttctgtct tctgttcttg tgattggaaa taagtggcac gccccattgc 60
 cttctagtcg ctcggcgaa gcgaagaggc cgaagcgaag aggcctggtg gttgtctca 120
 acatcctttt gctgagaatc gaatacgcag ccgatgaaca gccaggaagg gtgcaaggaa 180
 accttgaacg gcatctacca gttcatcatg gaccgcttcc ccttctaccg ggagaacaag 240
 cagggctggc agaacagcat ccgcacacaac ctctcgctca acgagtgtt cgtcaagggtg 300
 ccccgcgacg acaagaagcc cggcaag 327

<210> 12
 <211> 147
 <212> DNA
 <213> Homo sapiens

<400> 12
 ccgtctgaga atcgaataacg cagccgatga acagccagga agggtgcaag gaaaccttga 60
 acggcatcta ccagttcatc atggaccgct tccccttcta ccgggagaac aagcagggtc 120
 ggcagaacag catccgcccc aacctct 147

<210> 13
 <211> 878
 <212> DNA
 <213> Homo sapiens

<400> 13
 gtctctctca cttttctgtt cttgtatgaga cgaatttctt tccctcccc ttttccttcc 60
 tttggggcggtt gggagggtgg ataatatattt gggcgactcg atttaggtgt ttgtttttt 120
 gtttgggtgtt ttccccagat gacattgggtt taaaccggga caccctgtt aatacaaacg 180
 taggcagcaa ctgccatttt ggaattttt ttttcatatgt ccttagctat tttaggtttt 240
 gctgtgataa agctgtttt ctctctctt ctctctcaca cacacacaca caccctcg 300
 aaaagcagag taaaataatat tcccccagga agcctacagg ctgaggagtg tttcttgatc 360
 aatagttgc atttccagta aaatcgatgc acgaactcgat tttttttttt atgcgctgca 420
 ggagaaggc accttttgcgat agtcctttt tttttttttaag ctatgtcgaa aaataactagc 480
 ttatataaaa taataaaatgc atggggag ttttaggttg gggcagaaag ctcaaatcat 540
 ttgcgtgtga gctgagaact gggcagctt attttactttt gtttcaaaga aagaagaaaa 600
 agatcaggt tagaaaaaga gcccagaata ctcataaaaa caatgtttca gaagtggaaat 660
 attcaaggtt aaggAACCTG atttgtatct tccctttggc tttgaattgt tcaggagaca 720
 aagataatgc atctacatattt tcgtcttctg ttcttttattt ggaaataatgtt ggcacgcccc 780

attgccttct agtcgcctcc ccgaagcgaa gaggccgaag cgaagaggcc tggtggttg 840
 tctcaacatc ctttgctga gaatcgaata cgcagccg 878

<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 14 22
 ccattgcctt ctagtcgcot cc

<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 15 22
 cgttggggtc ggacacggag ta

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 16 27
 ggtacctacg cagccgatga acagcca

<210> 17
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 17 26
 gctagcgctg cttccgagac ggctcg

<210> 18
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 18 27
 ggtacccccc gagcctggaa actccct

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 19
 atgaacagcc aggaagggtg caagg

<210> 20
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 20
 acagccagga agggtgcaag gaaa

<210> 21
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 21
 gaagctgccg ttctcgaaca tggtg

<210> 22
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 22
 gtaggagtcc gggccagggttccag

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 23
 gcgttcggct cactgactta caagggt

<210> 24

25

24

25

25

26

<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for PCR

<400> 24
ggaagtgtct ctctcacctt ttctgtcttg a

31